

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Rine, Jasper D.
Boyartchuk, Victor L.
Ashby, Matthew N.
- (ii) TITLE OF INVENTION: AFC1 AND RCE1 ISOPRENYLATED CAAX
PROCESSING ENZYMES
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Pennie & Edmonds LLP
 - (B) STREET: 1155 Avenue of the Americas
 - (C) CITY: New York
 - (D) STATE: New York
 - (E) COUNTRY: USA
 - (F) ZIP: 10036
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Mandel, SaraLynn
 - (B) REGISTRATION NUMBER: 31,853
 - (C) REFERENCE/DOCKET NUMBER: 9067-008-999
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (415) 493-4935
 - (B) TELEFAX: (415) 493-5556
 - (C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1825 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ACCTACCTTT TTTTCTATCT TCAACAACGA AAGCCTTAC ACACACACAC ACATACATCT 60

ACATACATAC ATACAAATAT ACATATATGT AACTTGTAT ATTCATTCCT ATTAACCAAA 120

AAGAGGCAAT TAAACTTTTC CCTCTTTTTC TACGTCATTT ACTCAAAAAC TCTAATTCCT 180

TCGTCTCTGT TCTGCCATTT TCTCCAGAAA AATATCGACG GGAAATAAAA AAAAAAAGAC 240

AACGAACAAG AGAAAAAGTT CGCGAATTAT AAACCACTTC TATAATTAAC AGGAAAAGGA 300

AGGAAAAAAAA AGGAGGAAAA GAAAACTGCA GGCCTTTATT CATGTTTGAT CTTAAGACGA 360
 TTCTCGACCA TCCTAATATC CCGTGGAAT TAATCATTTT TGGGTTCTCG ATTGCCCAAT 420
 TTTCTTTTGA ATCTTACTTG ACGTACAGAC AGTACCAGAA GCTATCTGAA ACAAAGTTGC 480
 CACCTGTGCT GGAAGACGAA ATTGATGATG AAACCTTTTCA TAAATCAAGG AACTACTCCC 540
 GGGCCAAGGC CAAGTTCTCC ATTTTCGGTG ACGTCTATAA CCTAGCCCAA AAGCTAGTTT 600
 TCATCAAATA CGACCTCTTC CCTAAAATCT GGCACATGGC CGTTTCTTTA TTGAATGCAG 660
 TCCTGCCAGT CAGATTTTAT ATGGTCTCCA CTGTCGCACA GAGTTTTATG CTTCTTGGGT 720
 CTCTTATCCA GTTTGTCTAC CTTGGTTGAT TTGCCACTCT CTTACTATAG CCATTTTGTC 780
 CTGGAAGAAA AATTTGGTTT CAATAAATTG ACCGTCCAAC TATGGATCAC CGATATGATC 840
 AAGAGTCTGA CTTTGGCGTA TGCTATTGGT GGCCCAATCC TTTACCTGTT CCTTAAGATC 900
 TTTGATAAAT TCCCTACTGA TTTCCTTTGG TACATTATGG TCTTCTTGTT CGTTGTCCAA 960
 ATCTTAGCCA TGACAATCAT TCCAGTCTTC ATCATGCCCA TGTTTAATAA GTTCACTCCA 1020
 TTGGAGGACG GTGAACTGAA AAAATCTATT GAAAGTTTGG CCGATAGAGT TGGGTTCCCT 1080
 CTAGATAAGA TTTTGTTCAT TGACGGCTCA AAAAGATCTT CTCATTCAAA CGCATATTTT 1140
 ACAGGTTTGC CATTACCTC CAAGAGAATT GTTTTGTTCG ACACTTTAGT GAACAGTAAT 1200
 TCTACTGATG AAATTACGGC TGTTTTGGCC CATGAAATCG GTCAGTGGCA AAAAAACCAC 1260
 ATCGTTAATA TGGTCATCTT TAGTCAATTG CACACCTTCC TCATTTTCTC CCTTTTCACC 1320
 AGCATCTACA GAAATACATC ATTTTACAAC ACCTTCGGCT TTTTCTTAGA GAAGTCCACT 1380
 GGCAGTTTTG TTGATCCCGT TATCACTAAG GAATTCCCCA TTATCATTGG ATTTATGTTA 1440
 TTTAACGACT TATTAATCTC ACTCGAATGT GCCATGCAAT TCGTGATGAG TTTAATTTCC 1500
 AGAACTCATG AATATCAAGC TGATGCTTAT GCTAAAAAAT TGGGCTACAA GCAAAATCTA 1560
 TGTAGGGCTC TAATTGATCT ACAAATCAAA AACCTTTCCA CCATGAATGT AGATCCTCTG 1620
 TATTCTAGCT ATCATTATTC CCATCCAAC CTAGCTGAAA GATCGACCGC TCTAGACTAT 1680
 GTTAGTGAAA AGAAGAAAAA CTAATCTATA GAGTACACAT ATTAGCATGT ACCGTTAAAT 1740
 TCAGCTTCGT TATGTCTATA TCTACATACA TACACAGGTA TCTACTATAA GAATAAAGGA 1800
 AAGAAAAAAT AAACGATTAA ACATT 1825

2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2850 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TGAACTGTTG ATGAACAAAG AGAAGCTGAC AAGCATCAAA GCTTTGTACG ATGATTTCCA 60

TTCAAAAATT TGTGAATATG AAACCAAGTT CAACAAGAAT TTTCTTGAAT TAAATGAGTT 120
 ATATAATATG AATAGGGGAG ACCGTAGGCC AAAGGAACTG AAATTTACAG ATTTTATTAC 180
 TTCACAGCTG TTTAACGATA TCGAAAGCAT TTGCAACTTG AAAGTTAGTG TTCACAACTT 240
 ATCCAACATT TTTAAAAAAC AGGTCAGTAC CCTAAAACAA CACTCAAAGC ACGCATTATC 300
 TGAGGATTCA ATATCGCACA CAGGTAACGG TAGTTCATCG TCGCCCAGTT CAGCGTCATT 360
 AACGCCAGTA ACTTCTTCAT CCAAGAGTAG TTTATTTTTTA CCTAGCGGTA GCTCGTCTAC 420
 TTCCCTGAAA TTTACAGACC AGATTGTTCA TAAATGGGTT AGGATTGCTC CTTTACAGTA 480
 CAAACGAGAC ATTAATGTGA ACTTGGAAAT TAATAAGGAC ATTAAGGAAA CTTTAATTCC 540
 AAGTTTTGAA AGCTGCCTAT GTGTAGGTT TTATTGCGTT CGAGTAATGA TTAAATTTGA 600
 AAACCATCTT GCGTAGCGA AGATTGATAT CCCTATTTCT GTTAGGCAAG TGACAAAATA 660
 AAAAAACATT AGAAAAAATT CTCGTTACTT TTCTTATAGA TATAGATATA TGTATGGTTT 720
 GCTTATAGAT GAAGGTATTT ATCGCGTCTT TTGTATTCCC TATTATTAAT AAAATTCTTT 780
 TAAAATGCAT TTTCTGGTGC TCTTTTGTG CTCTGTATT TTTTTTTTTT TGGACCACTG 840
 GATGGAACAC CTTTGATGAT TTTATTACCT TTATTTTAAC TTAATAAAT ATCGAGATTT 900
 CAGGAACAAA ACATAGAATT TTCTTTGTCA AGAAAAATAA AACGAAATAA ATTGATGCTT 960
 TGACTACTGA CTGTCTGTCA TAGAGAGAAC CAGAACAGCA ATGCTACAAT TCTCAACATT 1020
 TCTAGTGCTC CTATACATCT CCATATCCTA TGTGCTACCG CTATATGCAA CTTCAACAAC 1080
 AGAAGGGTCT AAACGAGATA ATCCTCGAAC GATTAAATCT CGCATGCAA AACTTACAAT 1140
 TATGCTAATT TCCAACCTTT TTTTGGTGCC TTTTTTACAA TCTCAATTAT CTAGTACCAC 1200
 TTCACATATA AGTTTCAAGG ACGCATTTTT AGGCTTAGGT ATTATCCCAG GTTATTACGC 1260
 TGCATTGCCA AACCCTTGGC AATTCAGCCA GTTCGTGAAA GACTTAACGA AATGTGTTGC 1320
 GATGTTATTG ACCTTATATT GTGGACCCGT TTTAGATTTT GTATTATATC ATTTATTAAA 1380
 TCCAAAGAGC TCTATACTTG AAGATTTTTA CCATGAATTC CTGAATATTT GGAGTTTCAG 1440
 GAATTTTATA TTTGCACCAA TAACTGAGGA AATATTTTAC ACGTCAATGC TTTTGACTAC 1500
 GTACTTAAAC CTAATACCGC ATTCGCAACT AAGCTATCAA CAGTTATTTT GGCAACCATC 1560
 GCTTTTTTTT GGAATTGCGC ACGCACACCA TGCTTATGAG CAATTACAGG AAGGCTCCAT 1620
 GACAACGTGT TCCATTCTGC TGACAACATG CTTCCAAATT TTATACACAA CACTTTTTTG 1680
 AGGGTTAACC AAGTTTGTAT TGCAATATCA TGGGGTTTAA TGGTCCTTCA AGATTGAATT 1740
 TACATTTTAC AGTAGTAGAC AAGAAAGCTG GACGCATTTC CAAATTGGTC TCTCAATCTG 1800
 GAATAAGTGC TACTTCGCAC TGCTGGTCTT TGGATTAATA TCCCTGAAGG ATACCTTACA 1860
 AACTCTGGTA GGAACCTCTG GTTATAGAAT AACCCTTTAG CTTTTTTTAC GTACTTGTAT 1920
 ACCGTTTAAA ATTTCTATG TACTATAACC TTTTTCCTACT ACTATTATGG AATTCTATCG 1980
 AGCGACCGGG CTTTTGTTAC GGAAGAGTGA AAAAATCGAG TTTTGGTGTT TTGGTGAAAG 2040
 AATTTGGAGG ACTATAAGT ACCTATACTT TGTATTACGG ACTCAATAAC AAGTCGTTCC 2100

TGTCAGTGGT ATTGAAGTTG TCAGATCTAA GAGTAGAGAG AAGGTGGCAT CTAATAGGTT 2160
 TCGACGTTTT TCTTTTTTTA AGGTTTTTAT TTGGTCTCCT AGAATTTAAG GTCTTAGTTA 2220
 GTTTTGGTTT GTTTTGTGGG TTACATATTT TCAATTCAAA GGAGAATTTA GCTGTCTTTT 2280
 ATAATGTCCA ATAGAGATAA CGAGAGCATG CTGCGTACTA CATCAAGCGA TAAGGCGATC 2340
 GCTAGTCAAA GGGATAAACG GAAGTCTGAA GTTTTGATTG CTGCACAGTC CCTTGACAAT 2400
 GAAATCCGCA GCGTAAAAAA CCTAAAAAGA TTGTGCGATTG GGTCAATGGA TTTACTTATT 2460
 GATCCAGAAT TAGATATAAA ATTCGCTGGG GAATCTAGTG GGAGACGATC ATGGTCTGGC 2520
 ACGACATCCA GTTCTGCGTC AATGCCAAGT GACACAACCA CCGTTAATAA CACACGATAT 2580
 AGCGATCCAA CTCCGCTAGA GAACTTGCAT GGGAGGGGTA ACTCAGGGAT AGAATCCTCC 2640
 AATAAGACTA AAATTAAATG CTAACGTATT AAAGAAAAAC TTATTATGGG TTCCCGCCAA 2700
 TCAACACCCT AACGTTAAGC CTGATAATTT CCTAGAGCTT GTACAAGATA CTTTACAAAA 2760
 TATACAATA AGCGACAATG GTGAAGATAA TGATGGGAAT AGCAATGAAA ATAACGATAT 2820
 TGAGGATAAT GGGGAGGATA AAGAATCACA 2850

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..451
- (D) OTHER INFORMATION: /note= "The protein sequence of the Afclp protein from yeast presented as a polypeptide sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Phe Asp Leu Lys Thr Ile Leu Asp His Pro Asn Thr Pro Trp Lys
 1 5 10 15
 Leu Ile Ile Ser Gly Phe Ser Ile Ala Gln Phe Ser Phe Glu Ser Tyr
 20 25 30
 Leu Thr Tyr Arg Gln Tyr Gln Lys Leu Ser Glu Thr Lys Leu Pro Pro
 35 40 45
 Val Leu Glu Asp Glu Ile Asp Asp Glu Thr Phe His Lys Ser Arg Asn
 50 55 60
 Tyr Ser Arg Ala Lys Ala Lys Phe Ser Ile Phe Gly Asp Val Tyr Asn
 65 70 75 80
 Leu Ala Gln Lys Leu Val Phe Ile Lys Tyr Asp Leu Phe Pro Lys Ile
 85 90 95

Ser Glu Lys
450

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..315
- (D) OTHER INFORMATION: /note= "The sequence of the Rcelp protein from yeast presented as a polypeptide sequence."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Leu Gln Phe Ser Thr Phe Leu Val Leu Leu Tyr Ile Ser Ile Ser
1 5 10 15
Tyr Val Leu Pro Leu Tyr Ala Thr Ser Gln Pro Glu Gln Ser Lys Arg
20 25 30
Asp Asn Pro Arg Thr Ile Lys Ser Arg Met Gln Lys Leu Thr Ile Met
35 40 45
Leu Ile Ser Asn Leu Phe Leu Val Pro Phe Leu Gln Ser Gln Leu Ser
50 55 60
Ser Thr Thr Ser His Ile Gly Phe Lys Asp Ala Phe Leu Gly Leu Gly
65 70 75 80
Ile Ile Pro Gly Tyr Tyr Ala Ala Leu Pro Asn Pro Trp Gln Phe Ser
85 90 95
Gln Phe Val Lys Asp Leu Thr Lys Cys Val Ala Met Leu Leu Thr Leu
100 105 110
Tyr Cys Gly Pro Val Leu Asp Phe Val Leu Tyr His Leu Leu Asn Pro
115 120 125
Lys Ser Ser Ile Leu Glu Asp Phe Tyr His Glu Phe Leu Asn Ile Trp
130 135 140
Ser Phe Arg Asn Phe Ile Phe Ala Pro Ile Thr Glu Glu Ile Phe Tyr
145 150 155 160
Thr Ser Met Leu Leu Thr Thr Tyr Leu Asn Leu Ile Pro His Ser Gln
165 170 175
Leu Ser Tyr Gln Gln Leu Phe Trp Gln Pro Ser Leu Phe Phe Gly Leu
180 185 190
Ala His Ala His His Ala Tyr Glu Gln Leu Gln Glu Gly Ser Met Thr
195 200 205
Thr Val Ser Ile Leu Leu Thr Thr Cys Phe Gln Ile Leu Tyr Thr Thr
210 215 220

Sub
B1
cont

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